

### **INPUT SET: S32762.raw**

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**This Raw Listing contains the General Information Section and up to the first 5 pages.**

ENTERED

## SEQUENCE LISTING

2 (1) General Information:  
3  
4 (i) APPLICANT: PULST, STEFAN M.  
5  
6 (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR  
7 ATAXIA-2 AND PRODUCTS RELATED THERETO  
8  
9 (iii) NUMBER OF SEQUENCES: 18  
10  
11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.  
13 (B) STREET: 119 NORTH FOURTH STREET, SUITE 203  
14 (C) CITY: MINNEAPOLIS  
15 (D) STATE: MINNESOTA  
16 (E) COUNTRY: 55401  
17 (F) ZIP: 55401  
18  
19 (v) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Floppy disk  
21 (B) COMPUTER: IBM PC compatible  
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
24  
25 (vi) CURRENT APPLICATION DATA:  
26 (A) APPLICATION NUMBER: US 08/981,998  
27 (B) FILING DATE: 11-MAY-1998  
28 (C) CLASSIFICATION:  
29  
30 (vii) PRIOR APPLICATION DATA:  
31 (A) APPLICATION NUMBER: WO 97/42314  
32 (B) FILING DATE: 08-MAY-1997  
33  
34 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: US 08/727,084  
36 (B) FILING DATE: 08-OCT-1996  
37  
38 (vii) PRIOR APPLICATION DATA:  
39 (A) APPLICATION NUMBER: US 60/022,207  
40 (B) FILING DATE: 19-JUL-1996  
41  
42 (vii) PRIOR APPLICATION DATA:  
43 (A) APPLICATION NUMBER: US 60/017,388  
44 (B) FILING DATE: 08-MAY-1996  
45  
46

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47 (viii) ATTORNEY/AGENT INFORMATION:  
48 (A) NAME: MUETING, ANN M.  
49 (B) REGISTRATION NUMBER: 33,977  
50 (C) REFERENCE/DOCKET NUMBER: 232.00010120  
51

52 (ix) TELECOMMUNICATION INFORMATION:  
53 (A) TELEPHONE: 612-305-1217  
54 (B) TELEFAX: 612-305-1228  
55

56 (2) INFORMATION FOR SEQ ID NO:1:  
57

58 (i) SEQUENCE CHARACTERISTICS:  
59 (A) LENGTH: 516 base pairs  
60 (B) TYPE: nucleic acid  
61 (C) STRANDEDNESS: both  
62 (D) TOPOLOGY: both  
63

64 (ii) MOLECULE TYPE: DNA (genomic)  
65

66

67

68

69

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
71

72 TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCGG CTCCCGGCGG CTCCTTGGTC 60  
73 TCGGCGGGCC TCCCCGCCCC TTCGTGTCG TCCTTCTCCC CCTCGCCAGC CGGGGCGCCC 120  
75 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TGCCTCCCCG CCGCGTTCCG 180  
77 GCGTCTCCTT GGCGCGCCCG GCTCCCGGCT GTCCCCGCC 60  
78 GGCCTCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300  
80 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360  
82 AGCCCGGGCGG CAGCGGCCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCCG TCCTCGTCCT 420  
84 CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGGGCG 480  
86 88 GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCCC 516  
89

90 (2) INFORMATION FOR SEQ ID NO:2:  
91

92 (i) SEQUENCE CHARACTERISTICS:  
93 (A) LENGTH: 4481 base pairs  
94 (B) TYPE: nucleic acid  
95 (C) STRANDEDNESS: both  
96 (D) TOPOLOGY: both  
97

98 (ii) MOLECULE TYPE: cDNA  
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100  
 101 (ix) FEATURE:  
 102 (A) NAME/KEY: CDS  
 103 (B) LOCATION: 163..4101  
 104  
 105  
 106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
 107  
 108 ACCCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG 600  
 109  
 110 GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG 1200  
 111  
 112 CACCTCCGCT CCCACCCGGC GCCTCGGCCGC GCCCGCCCTC CG ATG CGC TCA GCG 1740  
 113 Met Arg Ser Ala  
 114 1  
 115  
 116  
 117 GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC 2220  
 118 Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe  
 119 5 10 15 20  
 120  
 121 GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG 2700  
 122 Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg  
 123 25 30 35  
 124  
 125 CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC 3180  
 126 Arg Ser Gly Arg Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser  
 127 40 45 50  
 128  
 129 GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG AGC 3660  
 130 Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln Ser  
 131 55 60 65  
 132  
 133 TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC 4140  
 134 Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly Gly  
 135 70 75 80  
 136  
 137 GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT 4620  
 138 Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Pro  
 139 85 90 95 100  
 140  
 141 CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC 5100  
 142 Pro Arg Pro Phe Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala  
 143 105 110 115  
 144  
 145 CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC 5580  
 146 Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser  
 147 120 125 130  
 148  
 149 CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC 6060  
 150 Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys Pro  
 151 135 140 145  
 152

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153	CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
154	Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
155	150 155 160	
156		
157	CCC CAG CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG	702
158	Pro Gln	
159	165 170 175 180	
160		
161	CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT GTC CGC	750
162	Gln Gln Gln Gln Gln Pro Pro Ala Ala Ala Asn Val Arg	
163	185 190 195	
164		
165	AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG CCT TCG	798
166	Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
167	200 205 210	
168		
169	CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC TCC TCG	846
170	Pro Ser Ser Ser Val Ser Ser Ser Ala Thr Ala Pro Ser Ser	
171	215 220 225	
172		
173		
174		
175	GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT	894
176	Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly	
177	230 235 240	
178		
179	CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA	942
180	Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly	
181	245 250 255 260	
182		
183	ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC	990
184	Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly	
185	265 270 275	
186		
187	TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT	1038
188	Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val	
189	280 285 290	
190		
191	TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT	1086
192	Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His	
193	295 300 305	
194		
195	GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG	1134
196	Glu Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met	
197	310 315 320	
198		
199	GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA	1182
200	Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys	
201	325 330 335 340	
202		
203	GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT	1230
204	Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala	
205	345 350 355	

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206	ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC	1278
207	Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro	
208	360 365 370	
209		
210		
211	TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA	1326
212	Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu	
213	375 380 385	
214		
215	AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT	1374
216	Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn	
217	390 395 400	
218		
219	GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG	1422
220	Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser	
221	405 410 415 420	
222		
223	TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG	1470
224	Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg	
225	425 430 435	
226		
227	GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT GCC CAG	1518
228	Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser Ala Gln	
229	440 445 450	
230		
231		
232		
233	TAC AAA GCT CGA GTG GCC CTG GAA AAT GAT GAT AGG AGT GAG GAA GAA	1566
234	Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu Glu Glu	
235	455 460 465	
236		
237	AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG CAC AGC	1614
238	Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly His Ser	
239	470 475 480	
240		
241	ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA AAT AGA	1662
242	Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg Asn Arg	
243	485 490 495 500	
244		
245	GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT ATG GGC	1710
246	Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg Met Gly	
247	505 510 515	
248		
249	CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC ACT TCA	1758
250	Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His Thr Ser	
251	520 525 530	
252		
253	GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT GGA GGT	1806
254	Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn Gly Gly	
255	535 540 545	
256		
257	GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA CCT TCT	1854
258	Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Arg Pro Pro Ser	

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